```
1    GAATTCCAGGCTGCTAGGAAGTGAAAAGTGAACCTGGACCCAGCTCAGCGGCAGCAGCAG    60

61   CGGCAGCAGGCAGCAGCCTCTATCCTCTCCTCCAGCCACATGGCCCCCGGATGGCGCTT   120
                                                MetGlyProArgMetAlaLeu

121  CCCCGCGTGCTCCTGCTCCTGTTCTTGCACCTGTTGCTGCTAGGATGCCGTTCCCATCCA   180
     ProArgValLeuLeuLeuLeuPheLeuHisLeuLeuLeuLeuGlyCysArgSerHisPro
     eProAlaCysSerCysSerCysSerCysThrCysCysCysEndAspAlaValProIleHi
     erProArgAlaProAlaProValLeuAlaProValAlaAlaArgMetProPheProSerT

181  CTGGGTGGCGCTGGCCTGGCCTCAGAACTGCCAGGGATACAGGTGAGCCCTGATGAACTG   240
     LeuGlyGlyAlaGlyLeuAlaSerGluLeuProGlyIleGlnValSerProAspGluLeu
     sTrpValAlaLeuAlaTrpProGlnAsnCysGlnGlyTyrArgEndAlaLeuMetAsnCy
     hrGlyTrpArgTrpProGlyLeuArgThrAlaArgAspThrGlyGluProEndEndThrA

241  CTTAGACTTGGTTGGCTGGGAGGGCGCGGACAGCAGCAACTAACGGGTCCCCACCTACTG   300
     LeuArgLeuGlyTrpLeuGlyGlyArgGlyGlnGlnGlnLeuThrGlyProHisLeuLeu
     sLeuAspLeuValGlyTrpGluGlyAlaAspSerSerAsnEndArgValProThrTyrCy
     laEndThrTrpLeuAlaGlyArgAlaArgThrAlaAlaThrAsnGlySerProProThrV
```

FIG. 1A

```
301  TTCCAAGAGGGCTCTAACCTCCTTTGGGAACTAGTGATAAGGGGTTTAGAAGGCAGCCAG  360
     PheGlnGluGlySerAsnLeuLeuTrpGluLeuValIleArgGlyLeuGluGlySerGln
     sSerLysArgAlaLeuThrSerPheGlyAsnEndEndEndGlyValEndLysAlaAlaAr
     alProArgGlyLeuEndProProLeuGlyThrSerAspLysGlyPheArgArgGlnProG

361  GCTGGGGGTGAGGACCCGCTCCCAAGGCAGTTGGTTCGCTTCAGCACCATCAAGAGTGAT  420
     AlaGlyGlyGluAspProLeuProArgGlnLeuValArgPheSerThrIleLysSerAsp
     gLeuGlyValArgThrArgSerGlnGlySerTrpPheAlaSerAlaProSerArgValMe
     lyTrpGlyEndGlyProAlaProLysAlaValGlySerLeuGlnHisHisGlnGluEndT

421  GGGTCCAGGTGCGAGTTCCTGAGGCTCGGGCTCCCCCACCCATCCCAGGAGCTGCTGGAC  480
     GlySerArgCysGluPheLeuArgLeuGlyLeuProHisProSerGlnGluLeuLeuAsp
     tGlyProGlyAlaSerSerEndGlySerGlySerProThrHisProArgSerCysTrpTh
     rpValGlnValArgValProGluAlaArgAlaProProProIleProGlyAlaAlaGlyP

481  CGCCTGCGAGACAGGGTCTCCGAGCTGCAGGCGACGGGACGGACCTGGAGCCCCTCCGGC  540
     ArgLeuArgAspArgValSerGluLeuGlnAlaThrGlyArgThrTrpSerProSerGly
     rAlaCysGluThrGlySerProSerCysArgArgArgAspGlyProGlyAlaProProAl
     roProAlaArgGlnGlyLeuArgAlaAlaGlyAspGlyThrAspLeuGluProLeuArgG

541  AGGACCGTGGCCTCACAGAAGCCTGGGAGGCGAGGGAAGCAGCCCCCACGGGGGTTCTTG  600
     ArgThrValAlaSerGlnLysProGlyArgArgGlyLysGlnProProArgGlyPheLeu
     aGlyProTrpProHisArgSerLeuGlyGlyGluGlySerSerProHisGlyGlySerTr
     lnAspArgGlyLeuThrGluAlaTrpGluAlaArgGluAlaAlaProThrGlyValLeuG
```

FIG. 1B

```
601  GGCCCCGCAGTAGCATCTTCCAAGTCCTCCGGGGAATACGCAGCCCCAAGACGATGCGTG   660
     GlyProAlaValAlaSerSerLysSerSer
     pAlaProGlnEndHisLeuProSerProPro
     lyProArgSerSerIlePheGlnValLeuArgGlyIleArgSerProLysThrMetArgA

661  ACTCTGGCTGCTTTGGGCGGAGGCTGGACCGGATCGGCTCCCTCAGCGGCCTGGGCTGCA   720
     spSerGlyCysPheGlyArgArgLeuAspArgIleGlySerLeuSerGlyLeuGlyCysA

721  ATGGTGAGCACCCACCCCATTCCCACTGCACGCCCCGGTTAGCATCACTTCTGGGTTTGA   780
     snV

781  TGTCTCTGGGACCAAACTCCGAGAAAAGGACACCTGGATATCACTCTTTCTTGTTGCCAG   840

841  TCCTCAAGGCCAAGGAGCGCCTTCCTGGAAAAATTAAATTTGGACAGCATTCACTAGCAT   900

901  GACTATGAGTCCCCACCCACCTTCTCGCCACCCCCTGCCTCTCTCACCCAAGGCGGCAGA   960

961  ATTACTTTAGGATGTAAATTCTGTCATTGCCTGGCTGCCGCTCCTGGGAGCAAAAAGAGA   1020
```

FIG.1C

```
1021  ACTAAACCTCTTCCCCCTGGTTTCCCCTCAACTGTCTGTGGCTGCAAAGGCAGAGGGCAG  1080

1081  GATCACCAGGGTGATGACAAGTCCCAGCTTACAAGGAGGAAACTCAGGTCCAGAGAGATG  1140

1141  GATTATCCCAAAGCCCCAAACATCCAGTTCTGCTGAAGAAGGCGGGTGGCAGGGGTGGCA  1200

1201  CGTGGTGGGGGGAAGCCCAGGTCCTGCCTGCCTCTCACCCTAATGTCATCCTCACCCTCT  1260

1261  CTCTCCCCCCCACAGTGCTCAGGAGGTACTGAGAAGTCCTGGCTGACAACCTCTGTGTCC  1320
                     alLeuArgArgTyr***

1321  GCTTCTCCAACGCCCCTCCCCTGCTCCCCTTCAAAGCAACTCCTGTTTTTATTTATGTAT  1380

1381  TTATTTATTTATTTATTTGGTGGTTGTATATAAGACGGTTCTTATTTGTGAGCACATTTT  1440

1441  TTCCATGGTGAAATAAAGTCAACATTAGAGCTCTGTCTTTTGAAAAAAAAAAAAAAAAGGA  1500

1501  ATTC  1504
```

FIG.1D

BNP Screening Oligos

```
5'-TCCAGCTGCTTCGGGGGCAGGATGGACAGGATTGGAGCCCAGAGCGGACTGGGCTGTAAC-3'  human ANP
   SerSerCysPheGlyGlyArgMetAspArgIleGlyAlaGlnSerGlyLeuGlyCysAsn-3'  human ANP
   (2)                                                     (21)
   SerGlyCysPheGlyArgArgLeuAspArgIleGlySerLeuSerGlyLeuGlyCysAsn     pig BNP
5'-ACNGGNTGCTTGGGNCGNCGNCTNGACCGNATNGGNTCNCTNTCNGGNCTNGGNTGCAAC-3'  Pig BNP
   TG      T  A   A  A  T   TA        AG T  AG    T      T  T

3'-AGGCCGACGAAGCCCGCGTCCGACCTGTCCTAACCTAGGGACTCGCCTGACCCGACATTG-5' 3351  (min:mal)

3'-TCGCCGACGAAGCCGTCTTCTGAGCTGTCTTAGCCGTCGGAGTCGCCGGAGCCGACGTTG-5' 3352  (G/T pref)

3'-AGGTCGACGAAGCCCCCGTCCTACCTGTCCTAACCTCGGGTCTCGCCTGACCCGACATTG-5' 3376  (ANP)
```

FIG.2

hn BNP cDNA (10-13-88)

```
1    GAATTCCAGGCTGCTAGGAAGTGAAAAGTGAACCTGGACCCAGCTCAGCGGCAGCAGCAGCGGCAGCAGG   70

71   CAGCAGCCTCTATCCTCTCCTCCAGCCACATGGGCCCCCGGATGGCGCTTCCCCGCGTGCTCCTGCTCCT   140
                                    MetGlyProArgMetAlaLeuProArgValLeuLeuLeuLe

141  GTTCTTGCACCTGTTGCTGCTAGGATGCCGTTCCCATCCACTGGGTGGCGCTGGCCTGGCCTCAGAACTG   210
     uPheLeuHisLeuLeuLeuLeuGlyCysArgSerHisProLeuGlyGlyAlaGlyLeuAlaSerGluLeu
                                  -1 +1                        10
211  CCAGGGATACAGGTGAGCCCTGATGAACTGCTTAGACTTGGTTGGCTGGGAGGGCGCGGACAGCAGCAAC   280
     ProGlyIleGln

281  TAACGGGTCCCCACCTACTGTTCCAAGAGGGCTCTAACCTCCTTTGGGAACTAGTGATAAGGGGTTAGAA   350

351  GGCAGCCAGGCTGGGGGTGAGGACCCCGCTCCCAAGGCAGTTGGTTCGCTTCAGCACCATCAAGAGTGAT   420

421  GGGTCCAGGTGCGAGTTCCTGAGGCTCGGGCTCCCCCACCCATCCCAGGAGCTGCTGGACCGCCTGCGAG   490
                                                      GluLeuLeuAspArgLeuArgA
                                                                     20.
491  ACAGGGTCTCCGAGCTGCAGGCGGAGCGGACGGACCTGGAGCCCCTCCGGCAGGACCGTGGCCTCACAGA   560
     spArgValSerGluLeuGlnAlaGluArgThrAspLeuGluProLeuArgGlnAspArgGlyLeuThrGl
                   30.                         40.
561  AGCCTGGGAGGCGAGGGAAGCAGCCCCCACGGGGTTCTTGGGCCCCGCAGTAGCATCTTCCAAGTCCTC   630
     uAlaTrpGluAlaArgGluAlaAlaProThrGlyValLeuGlyProArgSerSerIlePheGlnValLeu
```

FIG.3A

```
              50.        .        .       60.        .        .      70.
 631  CGGGGAATACGCAGCCCCAAGACGATGCGTGACTCTGGCTGCTTTGGGCGGAGGCTGGACCGGATCGGCT   700
      ArgGlyIleArgSerProLysThrMetArgAspSerGlyCysPheGlyArgArgLeuAspArgIleGlyS
            .  ↑1             80.↑2     .        .       90.        .
 701  CCCTCAGCGGCCTGGGCTGCAATGGTGAGCACCCACCCCCATTCCCACTGCACGCCCCGGTTAGCATCAC   770
      erLeuSerGlyLeuGlyCysAsnV
            .     100       .        .        .        .        .
 771  TTCTGGGTTTGATGTCTCTGGGGACCAAACTCCGAGAAAAGGACACCTGGATATCACTCTTTCTTGTTGC   840
            .        .        .        .        .        .        .
 841  CAGTCCTCAAGGCCAAGGAGCGCCTTCCTGGAAAAATTAAATTTGGACAGCATTCACTAGCATGACTATG   910
            .        .        .        .        .        .        .
 911  AGTCCCCACCCACCTTCTCGCCACCCCCTGCCTCTCTCACCCAAGGCGGCAGAATTACTTTAGGATGTAA   980
            .        .        .        .        .        .        .
 981  ATTCTGTCATTGCCTGGCTGCCGCTCCTGGGAGCAAAAAGAGAACTAAACCTCTTCCCCCTGGTTTCCCC  1050
            .        .        .        .        .        .        .
1051  TCAACTGTCTGTGGCTGCAAAGGCAGAGGGCAGGATCACCAGGGTGATGACAAGTCCCAGCTTACAAGGA  1120
            .        .        .        .        .        .        .
1121  GGAAACTCAGGTCCAGAGAGATGGATTATCCCAAAGCCCCAAACATCCAGTTCTGCTGAAGAAGGCGGGT  1190
            .        .        .        .        .        .        .
1191  GGCAGGGGTGGCACGTGGTGGGGGAAGCCCAGGTCCTGCCTGCCTCTCACCCTAATGTCATCCTCACCC  1260
            .        .        .        .        .        .        .
1261  TCTCTCTCCCCCCCACAGTGCTCAGGAGGTACTGAGAAGTCCTGGCTGACAACCTCTGTGTCCGCTTCTC  1330
                        alLeuArgArgTyr***
            .        .        106        .        .        .        .
1331  CAACGCCCCTCCCCTGCTCCCCTTCAAAGCAACTCCTGTTTTTATTTATGTATTTATTTATTTATTTATT  1400
            .        .        .        .        .        .        .
1401  TGGTGGTTGTATATAAGACGGTTCTTATTTGTGAGCACATTTTTTCCATGGTGAAATAAAGTCAACATTA  1470
            .        .        .
1471  GAGCTCTGTCTTTTGAAAAAAAAAAAAAAAGGAATTC  1507
```

FIG.3B

Mature Pig BNP cDNA (10-13-88)

```
  1  GAATTCCAGGCTGCTAGGAAGTGAAAAGTGAACCTGGACCCAGCTCAGCGGCAGCAGCAGCGGCAGCAGG   70

 71  CAGCAGCCTCTATCCTCTCCTCCAGCCACATGGGCCCCCGGATGGCGCTTCCCCGCGTGCTCCTGCTCCT  140
                                    MetGlyProArgMetAlaLeuProArgValLeuLeuLeuLe

141  GTTCTTGCACCTGTTGCTGCTAGGATGCCGTTCCCATCCACTGGGTGGCGCTGGCCTGGCCTCAGAACTG  210
     uPheLeuHisLeuLeuLeuLeuGlyCysArgSerHisProLeuGlyGlyAlaGlyLeuAlaSerGluLeu
          ↓1
211  CCAGGGATACAGGAGCTGCTGGACCGCCTGCGAGACAGGGTCTCCGAGCTGCAGGCGGAGCGGACGGACC  280
     ProGlyIleGlnGluLeuLeuAspArgLeuArgAspArgValSerGluLeuGlnAlaGluArgThrAspL

281  TGGAGCCCCTCCGGCAGGACCGTGGCCTCACAGAAGCCTGGGAGGCGAGGGAAGCAGCCCCCACGGGGGT  350
     euGluProLeuArgGlnAspArgGlyLeuThrGluAlaTrpGluAlaArgGluAlaAlaProThrGlyVa

351  TCTTGGGCCCCGCAGTAGCATCTTCCAAGTCCTCCGGGGAATACGCAGCCCCAAGACGATGCGTGACTCT  420
     lLeuGlyProArgSerSerIlePheGlnValLeuArgGlyIleArgSerProLysThrMetArgAspSer
                                                                ↓2
421  GGCTGCTTTGGGCGGAGGCTGGACCGGATCGGCTCCCTCAGCGGCCTGGGCTGCAATGTGCTCAGGAGGT  490
     GlyCysPheGlyArgArgLeuAspArgIleGlySerLeuSerGlyLeuGlyCysAsnValLeuArgArgT

491  ACTGAGAAGTCCTGGCTGACAACCTCTGTGTCCGCTTCTCCAACGCCCCTCCCCTGCTCCCCTTCAAAGC  560
     yr***

561  AACTCCTGTTTTTATTTATGTATTTATTTATTTATTTATTTGGTGGTTGTATATAAGACGGTTCTTATTT  630

631  GTGAGCACATTTTTTCCATGGTGAAATAAAGTCAACATTAGAGCTCTGTCTTTTGAAAAAAAAAAAAAAA  700

701  GGAATTC   707
```

FIG.4

Dog BNP Gene 12-12-88

```
  1  CGATCAGGGATGTTGGGGCGGAGGAAACGGAGGGAAGGAGGGAGCGGAGGAGGCCCGAGGACTGTTGGTG   70

 71  TCCCCCTCCTGCCCTTTTGGGGCCAGGCCCACTTCTATACAAGGCCTGCTCTCCAGCCTCCACCCCGGCG   140

141  GGTATGGTGCAGGCGCGGAGGGGCGCATTCCCCCGCCCTGAGCTCAGCGGCCGGAATGCGGCCGATAAAT   210

211  CAGAGATAACCCCAGGCGCGGGATAAGGGATAAAAAGCCCCCGTTGCCGCGGGATCCAGGAGAGCACCCG   280

281  CGCCCCAAGCGGTGACACTCGACCCCGGTCGCAGCGCAGCAGCTCAGCAGCCGGACGTCTCTTTCCCCAC   350

351  TTCTCTCCAGCGACATGGAGCCCTGCGCAGCGCTGCCCCGGGCCCTCCTGCTCCTCCTGTTCTTGCACCT   420
                   MetGluProCysAlaAlaLeuProArgAlaLeuLeuLeuLeuLeuPheLeuHisLe

421  GTCGCCACTCGGAGGCCGCCCCCACCCGCTGGGCGGCCGCAGCCCCGCCTCGGAAGCCTCGGAAGCCTCA   490
     uSerProLeuGlyGlyArgProHisProLeuGlyGlyArgSerProAlaSerGluAlaSerGluAlaSer

491  GAAGCCTCGGGGTTGTGGGCCGTGCAGGTGAGCGCTCAGCCTGCCTGAAGGCCGCGGCGGGTGGCAGCAG   560

561  GTCACGGGGGCTTAGCCACTGTCCCAAGTCCTCAGTCTCCCTTGGGAATTAGTGATAAGGGAATCAGAAA   630

631  GTGACGAGATTGGGTGCCAGGACTCCATACCCAAGGCGGCGGCTTCACTTGGGTGCAAGGGTGGTTCCGC   700

701  CCCGGCGTGGGTTCCTGAGGCTCAGGCCGTCCATTGCAGGAGCTGCTGGGCCGTCTGAAGGACGCAGTTT   770
                                            GluLeuLeuGlyArgLeuLysAspAlaValS
```

FIG.5A

771 CAGAGCTGCAGGCAGAGCAGTTGGCCCTGGAACCCCTGCACCGGAGCCACAGCCCCGCAGAAGCCCCGGA 840
erGluLeuGlnAlaGluGlnLeuAlaLeuGluProLeuHisArgSerHisSerProAlaGluAlaProGl

841 GGCCGGAGGAACGCCCCGTGGGGTCCTTGCACCCCATGACAGTGTCCTCCAGGCCCTGAGAAGACTACGC 910
uAlaGlyGlyThrProArgGlyValLeuAlaProHisAspSerValLeuGlnAlaLeuArgArgLeuArg

911 AGCCCCAAGATGATGCACAAGTCAGGGTGCTTTGGCCGGAGGCTGGACCGGATCGGCTCCCTCAGTGGCC 980
SerProLysMetMetHisLysSerGlyCysPheGlyArgArgLeuAspArgIleGlySerLeuSerGlyL

981 TGGGCTGCAATGGTAAGCCGCCTCCCTGCCGCCTTGGCTCCCCCTCCCCAGCCCCCTGGGTTCGACCCTT 1050
euGlyCysAsnV

1051 GGAACCCCTTCTGGGTTTGTTGTCTCGGGGGATCACACTCTGAGGAAAGGACATCTGGACATCGCTCCTT 1120

1121 CTTGCTGACAGTCCTAAGGGCCAAGGAGTACGTTTCTGGAAATACTACGTGTGGACATCGTTGTCCAGGG 1190

1191 TCCCTACCCACCTCCTAGCCCCCTCCTGCCTCTCGCACCCAAAGGGCAGAATCATCTTAGGATGGAATCA 1260

1261 GTCGTTGTCTGGAAGCATCTCCTTGGAGCAGAAAGAGTCCTAAACATCGTCCTCGTAGCTCTCTCTGTCT 1330

1331 GTCTGTAGCCACGAAGGCAGAGGTCAGGGTCACCAGGGCAGTGATGATTCCCAGTTAACAGAGGAGGAGA 1400

1401 CTGAGGTCTAGAGAGATGGATTATTCCAAAGCCTCAAACATCCAGATCGGCTGAGGGTGGGGTTGGTGGC 1470

1471 AGGGATGGCTCCTGGGCTTGGGAAGCTCGGATCCTGCCTCAGTCTCCCACCTGACGCCATCATCCCCCTC 1540

1541 TCTCTCCTCCCACAGTGCTGAGAAAGTATTAAGGAGGAAGTCCCGACTGCCCACATCTGCATTGGATTCT 1610

FIG.5B

alLeuArgLysTyr***

1611 TCAGCAGCCCCTGAGCCCCTTGGAAGCAGATCTTATTTATTCGTATTTATTTATTTATTTCGATTG 1680

1681 TTTTATATAAGATGATCCTGACGCCCGAGCACGGATTTTCCACGGTGAAATAAAGTCAACCTTAGAGCTT 1750

1751 CTTTTGAAACCGATTTGTCCCTGTGCATTAAAAGTAACACATCATTTAAAAAAA 1804

FIG.5C

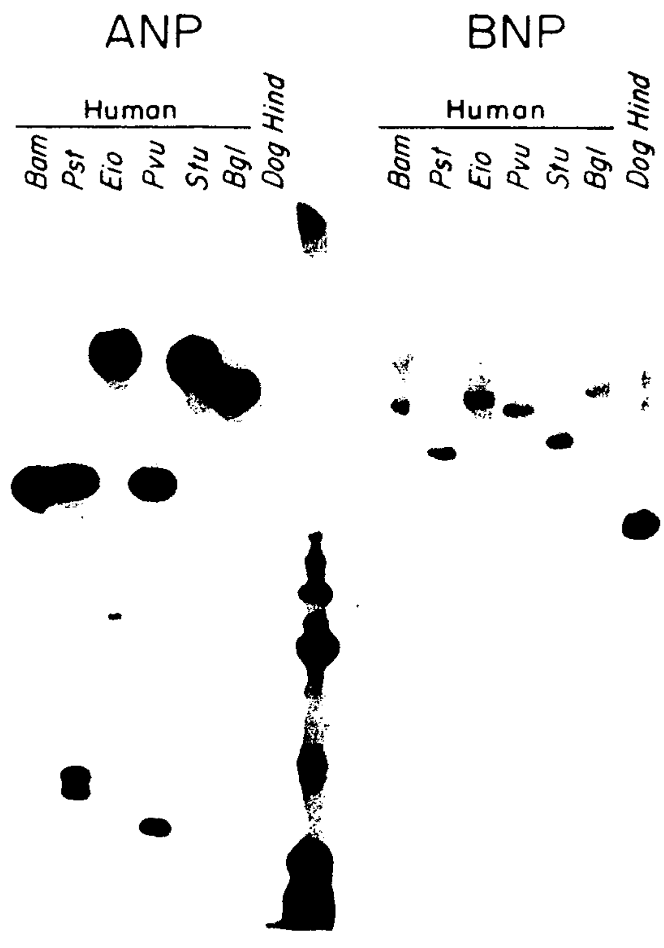
ANP
Human
Bam
Pst
Eio
Pvu
Stu
Bgl
Dog Hind
BNP
Human
Bam
Pst
Eio
Pvu
Stu
Bgl
Dog Hind

FIG.6

Human BNP Gene 12-12-88

```
  1  CCCACGGTGTCCCGAGGAGCCAGGAGGAGCACCCCGCAGGCTGAGGGCAGGTGGGAAGCAAACCCGGACG   70

 71  CATCGCAGCAGCAGCAGCAGCAGCAGAAGCAGCAGCAGCAGCCTCCGCAGTCCCTCCAGAGACATGGATC  140
                                                                    MetAspP

141  CCCAGACAGCACCTTCCCGGGCGCTCCTGCTCCTGCTCTTCTTGCATCTGGCTTTCCTGGGAGGTCGTTC  210
     roGlnThrAlaProSerArgAlaLeuLeuLeuLeuLeuPheLeuHisLeuAlaPheLeuGlyGlyArgSe

211  CCACCCGCTGGGCAGCCCCGGTTCAGCCTCGGACTTGGAAACGTCCGGGTTACAGGTGAGAGCGGAGGGC  280
     rHisProLeuGlySerProGlySerAlaSerAspLeuGluThrSerGlyLeuGln

281  AGCTCAGGGGGATTGGACAGCAGCAATGAAAGGGTCCTCACCTGCTGTCCCAAGAGGCCCTCATCTTTCC  350

351  TTTGGAATTAGTGATAAAGGAATCAGAAAATGGAGAGACTGGGTGCCCTGACCCTGTACCCAAGGCAGTC  420

421  GGTTCACTTGGGTGCCATGAAGGGCTGGTGAGCCAGGGGTGGGTCCCTGAGGCTTGGACGCCCCCATTCA  490

491  TTGCAGGAGCAGCGCAACCATTTGCAGGGCAAACTGTCGGAGCTGCAGGTGGAGCAGACATCCCTGGAGC  560
         GluGlnArgAsnHisLeuGlnGlyLysLeuSerGluLeuGlnValGluGlnThrSerLeuGluP

561  CCCTCCAGGAGAGCCCCCGTCCCACAGGTGTCTGGAAGTCCCGGGAGGTAGCCACCGAGGGCATCCGTGG  630
     roLeuGlnGluSerProArgProThrGlyValTrpLysSerArgGluValAlaThrGluGlyIleArgGl

631  GCACCGCAAAATGGTCCTCTACACCCTGCGGGCACCACGAAGCCCCAAGATGGTGCAAGGGTCTGGCTGC  700
     yHisArgLysMetValLeuTyrThrLeuArgAlaProArgSerProLysMetValGlnGlySerGlyCys
```

FIG.7A

```
701   TTTGGGAGGAAGATGGACCGGATCAGCTCCTCCAGTGGCCTGGGCTGCAAAGGTAAGCACCCCCTGCCAC   770
      PheGlyArgLysMetAspArgIleSerSerSerSerGlyLeuGlyCysLysV

771   CCCGGCCGCCTTCCCCCATTCCAGTGTGTGACACTGTTAGAGTCACTTTGGGGTTTGTTGTCTCTGGGAA   840

841   CCACACTCTTTGAGAAAAGGTCACCTGGACATCGCTTCCTCTTGTTAACAGCCTTCAGGGCCAAGGGGTG   910

911   CCTTTGTGGAATTAGTAAATGTGGGCTTATTTCATTACCATGCCCACAATACCTTCTCCCCACCTCCTAC   980

981   TTCTTATCAAAGGGGCAGAATCTCCTTTGGGGGTCTGTTTATCATTTGGCAGCCCCCCAGTGGTGCAGAA   1050

1051  AGAGAACCAAACATTTCCTCCTGGTTTCCTCTAAACTGTCTATAGTCTCAAAGGCAGAGAGCAGGATCAC   1120

1121  CAGAGCAATGATAATCCCCAATTTACAGATGAGGAAACTGAGGCTCAGAGAGTTGCATTAAGCCTCAAAC   1190

1191  GTCTGATGACTAACAGGGTGGTGGGTGGCACACGATGAGGTAAGCTCAGCCCCTGCCTCCATCTCCCACC   1260

1261  CTAACCATCATCACCCTCTCTCTTTCCCTGACAGTGCTGAGGCGGCATTAAGAGGAAGTCCTGGCTGCAG   1330
                                          alLeuArgArgHis***

1331  ACACCTGCTTCTGATTCCACAAGGGGCTTTTTCCTCAACCCTGTGGCCCTCATCTTTCCTTTGGAATTAG   1400

1401  TGATAAAGGAATCAGAAAATGGAGAGACTGGGTGCCCTGACCCTGTACCCAAGGCAGTCGGTTCACTTGG   1470

1471  GTGCCATGAAGGGCCTGGTGAGCCAGGGGTTGGGTCCCTGAGGCTTTTA   1519
```

FIG.7B

Pig PreproBNF
Dog PreproNRP
Human PreproNRP

```
                                     10                                      20
1  Met Gly Pro Arg Met Ala Leu Pro Arg Val Leu Leu Leu     Leu Phe Leu His Leu Leu Leu
2  --- Glu --- Cys Ala --- --- --- --- Ala --- --- --- Leu --- --- --- --- --- Ser Pro
3  --- Asp --- Gln Thr --- Pro Ser --- Ala --- --- --- --- --- --- --- --- --- Ala Phe
                                     30                                      40

   Leu Gly Cys Arg Ser His Pro Leu Gly Gly Ala Gly Leu Ala Ser Glu Leu Pro Gly Ile
   --- --- Gly --- Pro --- --- --- --- --- Arg Ser Pro --- --- --- Ala Ser Glu Ala
   --- --- Gly --- --- --- --- --- --- Ser Pro --- Ser --- --- Asp --- Glu Thr Ser
                       ↑SP
       ↓1                            50                                      60
   Gln Glu Leu Leu Asp Arg Leu Arg Asp Arg Val Ser Glu Leu Gln Ala Glu Arg Thr Asp
   Ser --- --- --- Gly --- --- Lys --- Ala --- --- --- --- --- --- --- Gln Leu Ala
   Gly --- Gln Arg Asn His --- Gln Gly Lys Leu --- --- --- --- Val --- Gln --- Ser
      ↑Leu Gln
                                     70                                      80
   Leu Glu Pro Leu Arg Gln Asp Arg Gly Leu Thr Glu Ala Trp Glu Ala Arg Glu Ala Ala
   --- --- --- --- --- His Arg Ser His Ser Pro Ala --- --- Pro --- --- Gly Gly Thr
   --- --- --- --- Gln Glu Ser Pro Arg Pro --- Gly Val --- Lys Ser --- --- Val ---

                                     90                                     100
   Pro Thr Gly Val Leu Gly Pro Arg Ser Ser Ile Phe Gln Val Leu Arg Gly Ile Arg Ser
   --- Arg --- --- --- Ala --- His Asp --- Val Leu --- Ala --- --- Arg Leu --- ---
   Thr Glu --- Ile Arg Gly His --- Lys Met Val Leu Tyr Thr --- --- Ala Pro --- ---
                                                                             ↑1
                                    110                                     120
   Pro Lys Thr Met Arg Asp Ser Gly Cys Phe Gly Arg Arg Leu Asp Arg Ile Gly Ser Leu
   --- --- Met --- His Lys --- --- --- --- --- --- --- --- --- --- --- --- --- ---
   --- --- Met Val Gln Gly --- --- --- --- --- --- Lys Met --- --- --- Ser --- Ser
           ↑?          ↑2
                                    130 131
   Ser Gly Leu Gly Cys Asn Val Leu Arg Arg Tyr
   --- --- --- --- --- --- --- --- --- Lys ---
   --- --- --- --- --- Lys --- --- --- --- His
```

FIG.8